AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (Withdrawn) Purified or isolated nucleic acid of the SPG4 gene, characterized in that it comprises a sequence chosen from the group comprising:

a) the sequence SEQ ID No. 1, the sequence SEQ ID No. 2, the sequence SEQ ID No. 72, the sequence SEQ ID No. 106 or the sequence of at least 15 consecutive nucleotides of one of these sequences;

b) the nucleic acid sequences which are homologs or variants of the sequences SEQ ID No. 1, SEQ ID No. 2, SEQ ID No. 72 or SEQ ID No. 106; and

c) the complementary sequence or the RNA sequence corresponding to the sequences as defined in a) and b).

2. (Withdrawn) Purified or isolated nucleic acid according to claim 1, with the exception of the nucleic acid identified in the GenBank databank under the accession number AB029006.

3. (Withdrawn) Purified or isolated nucleic acid according to claim 1, characterized in that it comprises at least one sequence of at least 15 consecutive nucleotides of the nt 714-809, ends inclusive, fragment of the sequence SEQ ID No. 2, of the sequence complementary thereto or of the sequence of the corresponding RNA thereof.

4. (Withdrawn) Purified or isolated nucleic acid according to claim 1, characterized in that it comprises a mutation corresponding to a natural polymorphism in humans.

5. (Withdrawn) Probe or primer, characterized in that it comprises a sequence of a nucleic acid according to claim 1.

6. (Withdrawn) Probe or primer according to claim 5, characterized in that its sequence is chosen from the sequences SEQ ID No. 4 to SEQ ID No. 71.

7. (Withdrawn) Splice acceptor or donor site, characterized in that it comprises a sequence of a nucleic acid according to claim 1 chosen from the sequences SEQ ID No. 74 to SEQ ID No. 105.

8. (Withdrawn) Method for screening cDNA or genomic DNA libraries, or for cloning isolated genomic or cDNA encoding spastin, characterized in that it uses a nucleic acid sequence according to claim 1.

9. ((Withdrawn) Method according to claim 8, for identifying the genomic or cDNA sequence of the SPG4 gene of mammals.

10-11. (Canceled)

12. (Withdrawn) Method for identifying the nucleic acid sequences which promote and/or regulate the expression of the SPG4 gene, characterized in that it uses a nucleic acid sequence according to claim 1.

13. (Withdrawn) Nucleic acid identified using a method according to claim 9.

14. (Withdrawn) Polypeptide encoded by a nucleic acid according to claim 1.

15. (Withdrawn) Polypeptide according to claim 14, with the exception of the 584 amino acid peptide, the sequence of which is identified in the GenBank databank under the accession number AB029006.

16. (Withdrawn) Polypeptide according to claim 14, characterized in that it comprises an amino acid sequence chosen from the group comprising:

a) the sequence SEQ ID No. 3, the sequence SEQ ID No. 73, the sequence SEQ ID No. 107 or the sequence of at least 10 consecutive amino acids of one of these sequences; and

b) the sequences which are homologs or variants of the sequences SEQ ID No. 3, SEQ ID No. 73 or SEQ ID No. 107.

17. (Withdrawn) Polypeptide according to claim 14, characterized in that it comprises the sequence of at least 8 consecutive amino acids of the sequence of the aa 197-228, ends inclusive, fragment of the sequence SEQ ID No. 3.

18. (Withdrawn) Polypeptide according to claim 14, characterized in that it comprises an amino acid sequence chosen from the group comprising the sequence SEQ ID No. 3, the sequence SEQ ID No. 73, the sequence SEQ ID No. 107, which sequences carrying at least one of the mutations corresponding to a natural polymorphism in humans, and the sequences of the fragments thereof of at least 10 consecutive amino acids.

19. (Withdrawn) Cloning and/or expression vector containing a nucleic acid sequence according to claim 1.

20. (Withdrawn) Vector according to claim 19, characterized in that it includes the elements required for its expression in a host cell.

21. (Withdrawn) Host cell transformed with a vector according to claim 19.

22. (Withdrawn) Mammal, except a human, characterized in that it comprises a cell according to claim 21.

23. (Withdrawn) Mammal, except a human, according to claim 22, comprising a transformed cell, characterized in that the sequence of at least one of the two alleles of the SPG4 gene contains at least one of the mutations corresponding to a natural polymorphism in humans.

24. (Withdrawn) The use of a nucleic acid sequence according to claim 5, as a probe or primer, for detecting and/or amplifying nucleic acid sequences.

25. (Withdrawn) The use of a nucleic acid sequence according to claim 1, for screening a genomic or cDNA library.

26. (Withdrawn) Use of a nucleic acid sequence according to claim 1, for producing a recombinant or synthetic polypeptide.

27. (Withdrawn) Method for producing a recombinant polypeptide, characterized in that a transformed cell according to claim 21 is cultured under conditions which allow the expression of said recombinant polypeptide, and in that said recombinant polypeptide is recovered.

28. (Withdrawn) Polypeptide, characterized in that it is obtained using a method according to claim 27.

29. (Withdrawn) Monoclonal or polyclonal antibodies or their fragments, chimeric antibodies or immunoconjugates, characterized in that they are capable of specifically recognizing a polypeptide according to claim 14.

30. (Withdrawn) Method for detecting and/or purifying a polypeptide, characterized in that it uses an antibody according to claim 29.

31. (Canceled)

32. (Currently Amended) A method for genotypic diagnosis of AD-HSP associated with the presence of at least one mutation on a sequence of the SPG4 gene, using a biological sample from a patient, characterized in that it includes the following steps:

a) where appropriate, isolation of the genomic DNA from the biological sample to be analyzed, or production of cDNA from the RNA of the biological sample;

b) specific amplification of said DNA sequence of the SPG4 gene likely to contain a mutation, using primers comprising a sequence selected from the group consisting of SEQ ID NO:1, at least 15 consecutive nucleotides of SEQ ID NO:1 and~~, a homolog of SEQ ID NO:1, a variant of SEQ ID NO:1~~, a sequence complementary to SEQ ID NO:1~~, an RNA sequence corresponding to SEQ ID NO:1, an RNA sequence corresponding to at least 15 consecutive nucleotides of SEQ ID NO:1, an RNA sequence corresponding to a homolog of SEQ ID NO:1, and an RNA sequence corresponding to a variant of SEQ ID NO:1~~;

c) analysis of the amplification products obtained and comparison of their sequence with the corresponding normal sequence of the SPG4 gene,

wherein, if the amplification products comprise a sequence associated with the presence of at least one mutation in a sequence of the SPG4 gene, AD-HSP is diagnosed in the patient.

33. (Withdrawn) Method for diagnosing AD-HSP associated with abnormal expression of a polypeptide encoded by the SPG4 gene, characterized in that one or more antibodies according to claim 29 is brought into contact with the biological material to be tested, under conditions which allow the possible formation of specific immunological complexes between said polypeptide and said antibody, and in that the immunological complexes possibly formed are detected and/or quantified.

34. (Withdrawn) Method for selecting a chemical or biochemical compound which is capable of modulating the expression or the activity of a polypeptide encoded by the 5PG4 gene, characterized in that it comprises bringing a nucleic acid sequence according to claim 1 into contact with a candidate compound, and detecting a modification of the activity of said polypeptide.

35. (Withdrawn) Use of a nucleic acid sequence according to claim 1, for studying the expression or the activity of the SPG4 gene.

36. (Withdrawn) Kit for diagnosis, characterized in that it comprises at least a nucleic acid according to claim 5.

37. (Withdrawn) Method for selecting a chemical or biochemical compound which is capable of modulating the expression or the activity of a polypeptide encoded by the SPG4 gene, characterized in that it comprises bringing a nucleic acid sequence according to claim 14 into contact with a candidate compound, and detecting a modification of the activity of said polypeptide.

38. (Withdrawn) Use of a polypeptide according to claim 14 for studying the expression or the activity of the SPG4 gene.

39. (Withdrawn) Kit for diagnosis, characterized in that it comprises at least an antibody according to claim 29.

40. (Withdrawn) Use of an antibody according to claim 29 for studying the expression or the activity of the SPG4 gene.

41. (Previously Presented) A method for detecting one or more polymorphisms in the SPG4 gene of a human biological sample, said method comprising:

a) amplifying SPG4 gene DNA of the sample thereby obtaining an amplification product,

b) sequencing the amplification product, thereby obtaining a DNA sequence of the amplification product; and

c) comparing the DNA sequence of the amplification product with the DNA sequence of a wild-type SPG4 gene;

whereby, if the DNA sequence of the amplification product is different from the DNA sequence of the wild-type SPG4 gene, then one or more polymorphisms in the SPG4 gene of the sample have been detected.

42. (Previously Presented) The method of claim 41, wherein the DNA is genomic DNA.

43. (Previously Presented) The method of claim 41, wherein the DNA is cDNA.

44. (Previously Presented) The method of claim 41, wherein the human biological sample is an antenatal human biological sample.

45. (Previously Presented) The method of claim 41, wherein the human biological sample comprises lymphoblasts.

46. (Previously Presented) The method of claim 41, wherein amplifying the DNA is performed by a method selected from the group consisting of: polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

47. (Currently Amended) A method for detecting one or more polymorphisms in the SPG4 gene of a human biological sample, said method comprising:

d) amplifying SPG4 gene DNA of the sample thereby obtaining an amplification product,

e) sequencing the amplification product, thereby obtaining a DNA sequence of the amplification product; and

f) comparing the DNA sequence of the amplification product with the DNA sequence of a wild-type SPG4 gene;

whereby, if the DNA sequence of the amplification product is different from the DNA sequence of the wild-type SPG4 gene, then one or more polymorphisms in the SPG4 gene of the sample have been detected,

wherein at least one primer is used, and wherein the primer comprises

~~The method of claim 41, which uses at least one primer comprising~~ any of the following:

the complement of nucleotides 383-405 of SEQ ID NO:1;

the complement of nucleotides 10278-10303 of SEQ ID NO:1;

the complement of nucleotides 10262-10236 of SEQ ID NO:1;

nucleotides 33728-33753 of SEQ ID NO:1;

nucleotides 35800-35826 of SEQ ID NO:1;

nucleotides 45058-45083 of SEQ ID NO:1;

nucleotides 62007-62031 of SEQ ID NO:1;

nucleotides 91208-91231 of SEQ ID NO:1;

nucleotides 100783-100808 of SEQ ID NO:1;

nucleotides 9976-9994 of SEQ ID NO:1;

the complement of nucleotides 35802-35821 of SEQ ID NO:1;

nucleotides 10037-10055 of SEQ ID NO:1;

the complement of nucleotides 35751-35770 of SEQ ID NO:1;

nucleotides 10418-10437 of SEQ ID NO:1;

the complement of nucleotides 62373-62390 of SEQ ID NO:1;

nucleotides 61968-61987 of SEQ ID NO:1;

the complement of nucleotides 91202-91220 of SEQ ID NO:1;

nucleotides 62008-62027 of SEQ ID NO:1;
the complement of nucleotides 91182-91201 of SEQ ID NO:1;
nucleotides 83346-83365 of SEQ ID NO:1;
the complement of nucleotides 101044-101062 of SEQ ID NO:1;
the complement of nucleotides 9638-9657 of SEQ ID NO:1;
the complement of nucleotides 10666-10686 of SEQ ID NO:1;
nucleotides 9658-9677 of SEQ ID NO:1;
the complement of nucleotides 10615-10633 of SEQ ID NO:1;
nucleotides 33230-33249 of SEQ ID NO:1;
the complement of nucleotides 33832-33853 of SEQ ID NO:1;
nucleotides 33251-33269 of SEQ ID NO:1;
nucleotides 35065-35085 of SEQ ID NO:1;
the complement of nucleotides 35857-35876 of SEQ ID NO:1;
nucleotides 44934-44953 of SEQ ID NO:1;
the complement of nucleotides 45293-45312 of SEQ ID NO:1;
the complement of nucleotides 45169-45186 of SEQ ID NO:1;
nucleotides 60684-60702 of SEQ ID NO:1;
the complement of nucleotides 61494-61513 of SEQ ID NO:1;
nucleotides 60707-60725 of SEQ ID NO:1;
nucleotides 61660-61679 of SEQ ID NO:1;
the complement of nucleotides 62124-62143 of SEQ ID NO:1;
nucleotides 62267-62285 of SEQ ID NO:1;
the complement of nucleotides 62667-62686 of SEQ ID NO:1;
nucleotides 73071-73090 of SEQ ID NO:1;
the complement of nucleotides 73697-73717 of SEQ ID NO:1;
nucleotides 74168-74187 of SEQ ID NO:1;
the complement of nucleotides 75416-75435 of SEQ ID NO:1;
nucleotides 74553-74574 of SEQ ID NO:1;
nucleotides 82534-82553 of SEQ ID NO:1;
nucleotides 82582-82601 of SEQ ID NO:1;
nucleotides 83044-83062 of SEQ ID NO:1;
the complement of nucleotides 83594-83615 of SEQ ID NO:1;

nucleotides 87840-87859 of SEQ ID NO:1;
the complement of nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 88206-88225 of SEQ ID NO:1;
nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 90165-90183 of SEQ ID NO:1;
the complement of nucleotides 89833-89852 of SEQ ID NO:1;
nucleotides 90619-90638 of SEQ ID NO:1;
the complement of nucleotides 91675-91694 of SEQ ID NO:1;
the complement of nucleotides 91285-91302 of SEQ ID NO:1;
nucleotides 93216-93236 of SEQ ID NO:1;
the complement of nucleotides 94601-94619 of SEQ ID NO:1;
nucleotides 93340-93360 of SEQ ID NO:1;
nucleotides 100421-100439 of SEQ ID NO:1; and
the complement of nucleotides 100846-100865 of SEQ ID NO:1.

48. (Previously Presented) A method for detecting one or more polymorphisms in the SPG4 gene of a human biological sample, said method comprising:

a) amplifying SPG4 gene DNA of the sample thereby obtaining an amplification product;

b) hybridizing the amplification product with a probe that hybridizes specifically with the DNA of a wild-type SPG4 gene, to produce a hybridized DNA; and

c) applying a method to detect one or more mismatches in the hybridized DNA;

whereby, if one or more mismatches are detected in the hybridized DNA, then one or more polymorphisms in the SPG4 gene of the sample have been detected.

49. (Previously Presented) The method of claim 48, wherein the DNA is genomic DNA.

50. (Previously Presented) The method of claim 48, wherein the DNA is cDNA.

51. (Previously Presented) The method of claim 48, wherein the human biological sample is an antenatal human biological sample.

52. (Previously Presented) The method of claim 48, wherein the human biological sample comprises lymphoblasts.

53. (Previously Presented) The method of claim 48, wherein amplifying the DNA is performed by a method selected from the group consisting of: polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

54. (Previously Presented) The method of claim 48, wherein the probe comprises any of the following:

the complement of nucleotides 383-405 of SEQ ID NO:1;

the complement of nucleotides 10278-10303 of SEQ ID NO:1;

the complement of nucleotides 10262-10236 of SEQ ID NO:1;

nucleotides 33728-33753 of SEQ ID NO:1;

nucleotides 35800-35826 of SEQ ID NO:1;

nucleotides 45058-45083 of SEQ ID NO:1;

nucleotides 62007-62031 of SEQ ID NO:1;

nucleotides 91208-91231 of SEQ ID NO:1;

nucleotides 100783-100808 of SEQ ID NO:1;

nucleotides 9976-9994 of SEQ ID NO:1;

the complement of nucleotides 35802-35821 of SEQ ID NO:1;

nucleotides 10037-10055 of SEQ ID NO:1;

the complement of nucleotides 35751-35770 of SEQ ID NO:1;

nucleotides 10418-10437 of SEQ ID NO:1;

the complement of nucleotides 62373-62390 of SEQ ID NO:1;
nucleotides 61968-61987 of SEQ ID NO:1;
the complement of nucleotides 91202-91220 of SEQ ID NO:1;
nucleotides 62008-62027 of SEQ ID NO:1;
the complement of nucleotides 91182-91201 of SEQ ID NO:1;
nucleotides 83346-83365 of SEQ ID NO:1;
the complement of nucleotides 101044-101062 of SEQ ID NO:1;
the complement of nucleotides 9638-9657 of SEQ ID NO:1;
the complement of nucleotides 10666-10686 of SEQ ID NO:1;
nucleotides 9658-9677 of SEQ ID NO:1;
the complement of nucleotides 10615-10633 of SEQ ID NO:1;
nucleotides 33230-33249 of SEQ ID NO:1;
the complement of nucleotides 33832-33853 of SEQ ID NO:1;
nucleotides 33251-33269 of SEQ ID NO:1;
nucleotides 35065-35085 of SEQ ID NO:1;
the complement of nucleotides 35857-35876 of SEQ ID NO:1;
nucleotides 44934-44953 of SEQ ID NO:1;
the complement of nucleotides 45293-45312 of SEQ ID NO:1;
the complement of nucleotides 45169-45186 of SEQ ID NO:1;
nucleotides 60684-60702 of SEQ ID NO:1;
the complement of nucleotides 61494-61513 of SEQ ID NO:1;
nucleotides 60707-60725 of SEQ ID NO:1;
nucleotides 61660-61679 of SEQ ID NO:1;
the complement of nucleotides 62124-62143 of SEQ ID NO:1;
nucleotides 62267-62285 of SEQ ID NO:1;
the complement of nucleotides 62667-62686 of SEQ ID NO:1;
nucleotides 73071-73090 of SEQ ID NO:1;
the complement of nucleotides 73697-73717 of SEQ ID NO:1;
nucleotides 74168-74187 of SEQ ID NO:1;
the complement of nucleotides 75416-75435 of SEQ ID NO:1;
nucleotides 74553-74574 of SEQ ID NO:1;
nucleotides 82534-82553 of SEQ ID NO:1;

nucleotides 82582-82601 of SEQ ID NO:1;
nucleotides 83044-83062 of SEQ ID NO:1;
the complement of nucleotides 83594-83615 of SEQ ID NO:1;
nucleotides 87840-87859 of SEQ ID NO:1;
the complement of nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 88206-88225 of SEQ ID NO:1;
nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 90165-90183 of SEQ ID NO:1;
the complement of nucleotides 89833-89852 of SEQ ID NO:1;
nucleotides 90619-90638 of SEQ ID NO:1;
the complement of nucleotides 91675-91694 of SEQ ID NO:1;
the complement of nucleotides 91285-91302 of SEQ ID NO:1;
nucleotides 93216-93236 of SEQ ID NO:1;
the complement of nucleotides 94601-94619 of SEQ ID NO:1;
nucleotides 93340-93360 of SEQ ID NO:1;
nucleotides 100421-100439 of SEQ ID NO:1; and
the complement of nucleotides 100846-100865 of SEQ ID NO:1.

55. (Previously Presented) A method for diagnosing the presence or absence of an autosomal dominant hereditary spastic paraplegia in a human, wherein the autosomal dominant hereditary spastic paraplegia is associated with the presence of a mutation in the SPG4 gene, the method comprising detecting the presence or absence of one or more mutations in the SPG4 gene in a biological sample obtained from the human, wherein if the biological sample comprises a sequence associated with the presence of at least one mutation in the SPG4 gene, an autosomal dominant hereditary spastic paraplegia is diagnosed in the human.

56. (Previously Presented) The method of claim 55 wherein detecting the presence or absence of one or more mutations in the SPG4 gene comprises amplifying DNA of the biological sample obtained from the human using primers, determining the DNA sequence of the amplified product, and comparing the DNA

sequence of the amplified product with the DNA sequence of a wild-type SPG4 gene to detect one or more mutations in the SPG4 gene in the biological sample.

57. (Previously Presented) The method of claim 56, wherein the DNA is genomic DNA.

58. (Previously Presented) The method of claim 56, wherein the DNA is cDNA.

59. (Previously Presented) The method of claim 56, wherein the biological sample is an antenatal human biological sample.

60. (Previously Presented) The method of claim 56, wherein the biological sample comprises lymphoblasts.

61. (Previously Presented) The method of claim 56, wherein amplifying the DNA is performed by a method selected from the group consisting of: polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

62. (Previously Presented) The method of claim 56, which uses at least one primer comprising any of the following:

the complement of nucleotides 383-405 of SEQ ID NO:1;
the complement of nucleotides 10278-10303 of SEQ ID NO:1;
the complement of nucleotides 10262-10236 of SEQ ID NO:1;
nucleotides 33728-33753 of SEQ ID NO:1;
nucleotides 35800-35826 of SEQ ID NO:1;
nucleotides 45058-45083 of SEQ ID NO:1;
nucleotides 62007-62031 of SEQ ID NO:1;
nucleotides 91208-91231 of SEQ ID NO:1;

nucleotides 100783-100808 of SEQ ID NO:1;
nucleotides 9976-9994 of SEQ ID NO:1;
the complement of nucleotides 35802-35821 of SEQ ID NO:1;
nucleotides 10037-10055 of SEQ ID NO:1;
the complement of nucleotides 35751-35770 of SEQ ID NO:1;
nucleotides 10418-10437 of SEQ ID NO:1;
the complement of nucleotides 62373-62390 of SEQ ID NO:1;
nucleotides 61968-61987 of SEQ ID NO:1;
the complement of nucleotides 91202-91220 of SEQ ID NO:1;
nucleotides 62008-62027 of SEQ ID NO:1;
the complement of nucleotides 91182-91201 of SEQ ID NO:1;
nucleotides 83346-83365 of SEQ ID NO:1;
the complement of nucleotides 101044-101062 of SEQ ID NO:1;
the complement of nucleotides 9638-9657 of SEQ ID NO:1;
the complement of nucleotides 10666-10686 of SEQ ID NO:1;
nucleotides 9658-9677 of SEQ ID NO:1;
the complement of nucleotides 10615-10633 of SEQ ID NO:1;
nucleotides 33230-33249 of SEQ ID NO:1;
the complement of nucleotides 33832-33853 of SEQ ID NO:1;
nucleotides 33251-33269 of SEQ ID NO:1;
nucleotides 35065-35085 of SEQ ID NO:1;
the complement of nucleotides 35857-35876 of SEQ ID NO:1;
nucleotides 44934-44953 of SEQ ID NO:1;
the complement of nucleotides 45293-45312 of SEQ ID NO:1;
the complement of nucleotides 45169-45186 of SEQ ID NO:1;
nucleotides 60684-60702 of SEQ ID NO:1;
the complement of nucleotides 61494-61513 of SEQ ID NO:1;
nucleotides 60707-60725 of SEQ ID NO:1;
nucleotides 61660-61679 of SEQ ID NO:1;
the complement of nucleotides 62124-62143 of SEQ ID NO:1;
nucleotides 62267-62285 of SEQ ID NO:1;
the complement of nucleotides 62667-62686 of SEQ ID NO:1;

nucleotides 73071-73090 of SEQ ID NO:1;
the complement of nucleotides 73697-73717 of SEQ ID NO:1;
nucleotides 74168-74187 of SEQ ID NO:1;
the complement of nucleotides 75416-75435 of SEQ ID NO:1;
nucleotides 74553-74574 of SEQ ID NO:1;
nucleotides 82534-82553 of SEQ ID NO:1;
nucleotides 82582-82601 of SEQ ID NO:1;
nucleotides 83044-83062 of SEQ ID NO:1;
the complement of nucleotides 83594-83615 of SEQ ID NO:1;
nucleotides 87840-87859 of SEQ ID NO:1;
the complement of nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 88206-88225 of SEQ ID NO:1;
nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 90165-90183 of SEQ ID NO:1;
the complement of nucleotides 89833-89852 of SEQ ID NO:1;
nucleotides 90619-90638 of SEQ ID NO:1;
the complement of nucleotides 91675-91694 of SEQ ID NO:1;
the complement of nucleotides 91285-91302 of SEQ ID NO:1;
nucleotides 93216-93236 of SEQ ID NO:1;
the complement of nucleotides 94601-94619 of SEQ ID NO:1;
nucleotides 93340-93360 of SEQ ID NO:1;
nucleotides 100421-100439 of SEQ ID NO:1; and
the complement of nucleotides 100846-100865 of SEQ ID NO:1.

63. (Previously Presented) The method of claim 55, wherein detecting the presence or absence of a mutation in the SPG4 gene comprises amplifying DNA of the biological sample obtained from the human, hybridizing the amplified product with a probe that hybridizes specifically with the DNA of a wild-type SPG4 gene, applying a method to detect the presence of one or more mismatches in the hybridized DNA, wherein the detection of one or more mismatches indicates one or more mutations in the SPG4 gene in the biological sample.

64. (Previously Presented) The method of claim 63, wherein the DNA is genomic DNA.

65. (Previously Presented) The method of claim 63, wherein the DNA is cDNA.

66. (Previously Presented) The method of claim 63, wherein the biological sample is an antenatal human biological sample.

67. (Previously Presented) The method of claim 63, wherein the biological sample comprises lymphoblasts.

68. (Previously Presented) The method of claim 63, wherein amplifying the DNA is performed by a method selected from the group consisting of: polymerase chain reaction, strand displacement amplification, transcription-based amplification system, self-sustained sequence replication, nucleic acid sequence based amplification, transcription mediated amplification, ligase chain reaction, repair chain reaction and cycling probe reaction.

69. (Previously Presented) The method of claim 63, which uses at least one probe comprising any of the following:

the complement of nucleotides 383-405 of SEQ ID NO:1;
the complement of nucleotides 10278-10303 of SEQ ID NO:1;
the complement of nucleotides 10262-10236 of SEQ ID NO:1;
nucleotides 33728-33753 of SEQ ID NO:1;
nucleotides 35800-35826 of SEQ ID NO:1;
nucleotides 45058-45083 of SEQ ID NO:1;
nucleotides 62007-62031 of SEQ ID NO:1;
nucleotides 91208-91231 of SEQ ID NO:1;
nucleotides 100783-100808 of SEQ ID NO:1;
nucleotides 9976-9994 of SEQ ID NO:1;
the complement of nucleotides 35802-35821 of SEQ ID NO:1;

nucleotides 10037-10055 of SEQ ID NO:1;
the complement of nucleotides 35751-35770 of SEQ ID NO:1;
nucleotides 10418-10437 of SEQ ID NO:1;
the complement of nucleotides 62373-62390 of SEQ ID NO:1;
nucleotides 61968-61987 of SEQ ID NO:1;
the complement of nucleotides 91202-91220 of SEQ ID NO:1;
nucleotides 62008-62027 of SEQ ID NO:1;
the complement of nucleotides 91182-91201 of SEQ ID NO:1;
nucleotides 83346-83365 of SEQ ID NO:1;
the complement of nucleotides 101044-101062 of SEQ ID NO:1;
the complement of nucleotides 9638-9657 of SEQ ID NO:1;
the complement of nucleotides 10666-10686 of SEQ ID NO:1;
nucleotides 9658-9677 of SEQ ID NO:1;
the complement of nucleotides 10615-10633 of SEQ ID NO:1;
nucleotides 33230-33249 of SEQ ID NO:1;
the complement of nucleotides 33832-33853 of SEQ ID NO:1;
nucleotides 33251-33269 of SEQ ID NO:1;
nucleotides 35065-35085 of SEQ ID NO:1;
the complement of nucleotides 35857-35876 of SEQ ID NO:1;
nucleotides 44934-44953 of SEQ ID NO:1;
the complement of nucleotides 45293-45312 of SEQ ID NO:1;
the complement of nucleotides 45169-45186 of SEQ ID NO:1;
nucleotides 60684-60702 of SEQ ID NO:1;
the complement of nucleotides 61494-61513 of SEQ ID NO:1;
nucleotides 60707-60725 of SEQ ID NO:1;
nucleotides 61660-61679 of SEQ ID NO:1;
the complement of nucleotides 62124-62143 of SEQ ID NO:1;
nucleotides 62267-62285 of SEQ ID NO:1;
the complement of nucleotides 62667-62686 of SEQ ID NO:1;
nucleotides 73071-73090 of SEQ ID NO:1;
the complement of nucleotides 73697-73717 of SEQ ID NO:1;
nucleotides 74168-74187 of SEQ ID NO:1;

the complement of nucleotides 75416-75435 of SEQ ID NO:1;
nucleotides 74553-74574 of SEQ ID NO:1;
nucleotides 82534-82553 of SEQ ID NO:1;
nucleotides 82582-82601 of SEQ ID NO:1;
nucleotides 83044-83062 of SEQ ID NO:1;
the complement of nucleotides 83594-83615 of SEQ ID NO:1;
nucleotides 87840-87859 of SEQ ID NO:1;
the complement of nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 88206-88225 of SEQ ID NO:1;
nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 90165-90183 of SEQ ID NO:1;
the complement of nucleotides 89833-89852 of SEQ ID NO:1;
nucleotides 90619-90638 of SEQ ID NO:1;
the complement of nucleotides 91675-91694 of SEQ ID NO:1;
the complement of nucleotides 91285-91302 of SEQ ID NO:1;
nucleotides 93216-93236 of SEQ ID NO:1;
the complement of nucleotides 94601-94619 of SEQ ID NO:1;
nucleotides 93340-93360 of SEQ ID NO:1;
nucleotides 100421-100439 of SEQ ID NO:1; and
the complement of nucleotides 100846-100865 of SEQ ID NO:1.

70. (Canceled)

71. (Previously Presented) The method of claim 55, wherein the mutation is detected using at least one nucleic acid comprising any of the following:
the complement of nucleotides 383-405 of SEQ ID NO:1;
the complement of nucleotides 10278-10303 of SEQ ID NO:1;
the complement of nucleotides 10262-10236 of SEQ ID NO:1;
nucleotides 33728-33753 of SEQ ID NO:1;
nucleotides 35800-35826 of SEQ ID NO:1;
nucleotides 45058-45083 of SEQ ID NO:1;
nucleotides 62007-62031 of SEQ ID NO:1;

nucleotides 91208-91231 of SEQ ID NO:1;
nucleotides 100783-100808 of SEQ ID NO:1;
nucleotides 9976-9994 of SEQ ID NO:1;
the complement of nucleotides 35802-35821 of SEQ ID NO:1;
nucleotides 10037-10055 of SEQ ID NO:1;
the complement of nucleotides 35751-35770 of SEQ ID NO:1;
nucleotides 10418-10437 of SEQ ID NO:1;
the complement of nucleotides 62373-62390 of SEQ ID NO:1;
nucleotides 61968-61987 of SEQ ID NO:1;
the complement of nucleotides 91202-91220 of SEQ ID NO:1;
nucleotides 62008-62027 of SEQ ID NO:1;
the complement of nucleotides 91182-91201 of SEQ ID NO:1;
nucleotides 83346-83365 of SEQ ID NO:1;
the complement of nucleotides 101044-101062 of SEQ ID NO:1;
the complement of nucleotides 9638-9657 of SEQ ID NO:1;
the complement of nucleotides 10666-10686 of SEQ ID NO:1;
nucleotides 9658-9677 of SEQ ID NO:1;
the complement of nucleotides 10615-10633 of SEQ ID NO:1;
nucleotides 33230-33249 of SEQ ID NO:1;
the complement of nucleotides 33832-33853 of SEQ ID NO:1;
nucleotides 33251-33269 of SEQ ID NO:1;
nucleotides 35065-35085 of SEQ ID NO:1;
the complement of nucleotides 35857-35876 of SEQ ID NO:1;
nucleotides 44934-44953 of SEQ ID NO:1;
the complement of nucleotides 45293-45312 of SEQ ID NO:1;
the complement of nucleotides 45169-45186 of SEQ ID NO:1;
nucleotides 60684-60702 of SEQ ID NO:1;
the complement of nucleotides 61494-61513 of SEQ ID NO:1;
nucleotides 60707-60725 of SEQ ID NO:1;
nucleotides 61660-61679 of SEQ ID NO:1;
the complement of nucleotides 62124-62143 of SEQ ID NO:1;
nucleotides 62267-62285 of SEQ ID NO:1;

the complement of nucleotides 62667-62686 of SEQ ID NO:1;
nucleotides 73071-73090 of SEQ ID NO:1;
the complement of nucleotides 73697-73717 of SEQ ID NO:1;
nucleotides 74168-74187 of SEQ ID NO:1;
the complement of nucleotides 75416-75435 of SEQ ID NO:1;
nucleotides 74553-74574 of SEQ ID NO:1;
nucleotides 82534-82553 of SEQ ID NO:1;
nucleotides 82582-82601 of SEQ ID NO:1;
nucleotides 83044-83062 of SEQ ID NO:1;
the complement of nucleotides 83594-83615 of SEQ ID NO:1;
nucleotides 87840-87859 of SEQ ID NO:1;
the complement of nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 88206-88225 of SEQ ID NO:1;
nucleotides 89181-89200 of SEQ ID NO:1;
the complement of nucleotides 90165-90183 of SEQ ID NO:1;
the complement of nucleotides 89833-89852 of SEQ ID NO:1;
nucleotides 90619-90638 of SEQ ID NO:1;
the complement of nucleotides 91675-91694 of SEQ ID NO:1;
the complement of nucleotides 91285-91302 of SEQ ID NO:1;
nucleotides 93216-93236 of SEQ ID NO:1;
the complement of nucleotides 94601-94619 of SEQ ID NO:1;
nucleotides 93340-93360 of SEQ ID NO:1;
nucleotides 100421-100439 of SEQ ID NO:1; and
the complement of nucleotides 100846-100865 of SEQ ID NO:1.